09/607853

WEST

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Term: Transposable element near5 amplif$

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Search History

DATE: Wednesday, June 26, 2002 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=DWPI,USPT,EPAB,JPAB; PLUR=YES; OP=ADJ			
L1	Transposable element near5 amplif$	13	L1

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Your wildcard search against 2000 terms has yielded the results below

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Search Results - Record(s) 1 through 10 of 13 returned.

☐ 1. 6300542 . 24 May 99; 09 Oct 01. Functional characterization of genes. Briggs; Steven P., et al. 800/267; 800/278. A01H001/00 A01H001/02.

☐ 2. 6297426 . 14 Apr 98; 02 Oct 01. Methods of mediating female fertility in plants. Albertsen; Marc C., et al. 800/278; 435/410 435/468 800/271 800/290 800/298. A01H005/00 A01H004/00 C12N015/00 C12N015/05.

☑ 3. 6265640 . 10 Dec 98; 24 Jul 01. Nucleotide sequences mediating fertility and method of using same. Albertsen; Marc C., et al. 800/303; 536/23.7 536/24.1 800/271 800/275 800/298. A01H005/00 A01H004/00 C12N005/04.

☑ 4. 5962764 . 10 Apr 97; 05 Oct 99. Functional characterization of genes. Briggs; Steven P., et al. 800/270; 536/23.6 536/24.1 536/24.33 800/267 800/275 800/298 800/320.1. A01H004/00 C12N015/09.

☐ 5. 5861273 . 07 Jun 95; 19 Jan 99. Chromosomal expression of heterologous genes in bacterial cells. Olson; Pamela S., et al. 435/69.1; 435/252.33 435/320.1 536/23.1 536/24.1. C12P021/02 C12N001/21 C12N015/64 C12N015/70.

☐ 6. 5859341 . 07 Jun 95; 12 Jan 99. Nucleotide sequences mediating fertility and method of using same. Albertsen; Marc C., et al. 800/271; 47/DIG.1 536/23.1 536/23.6 800/274 800/278 800/298 800/303. A01H005/00 A01H004/00 C12N015/00 C12N015/05.

☐ 7. 5850014 . 07 Jun 95; 15 Dec 98. Nucleotide sequences mediating ferility and method of using same. Albertsen; Marc C., et al. 800/298; 47/DIG.1 536/23.1 536/23.6 800/291 800/303. C12N015/00 C12N005/00 A01H001/06 A01H004/00.

☐ 8. 5824524 . 07 Jun 95; 20 Oct 98. Nucleotide sequences mediating fertility and method of using same. Albertsen; Marc C., et al. 800/270; 47/DIG.1 536/23.1 536/23.6 536/24.1 800/274 800/275 800/278 800/286. C12N015/00 C12N015/05 A01H001/00.

☐ 9. 5478369 . 02 Aug 93; 26 Dec 95. Nucleotide sequences mediating male fertility and method of using same. Albertsen; Marc C., et al. 800/275; 47/DIG.1 536/23.1 536/23.6 800/276 800/286. A01H001/00 C12N015/11 C12N015/82.

☐ 10. 5470724 . 19 Jan 94; 28 Nov 95. Boomerang DNA amplification. Ahern; Kevin G.. 435/91.2; 536/24.2 536/24.3. C12P019/34.

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Term	Documents
TRANSPOSABLE.DWPI,EPAB,JPAB,USPT.	995
TRANSPOSABLES	0
ELEMENT.DWPI,EPAB,JPAB,USPT.	2160656
ELEMENTS.DWPI,EPAB,JPAB,USPT.	1793935
AMPLIF$	0
AMPLIF.DWPI,EPAB,JPAB,USPT.	77
AMPLIFABLE.DWPI,EPAB,JPAB,USPT.	4
AMPLIFACATION.DWPI,EPAB,JPAB,USPT.	2
AMPLIFACTION.DWPI,EPAB,JPAB,USPT.	6
AMPLIFACTIONS:.DWPI,EPAB,JPAB,USPT.	1
AMPLIFACTORY.DWPI,EPAB,JPAB,USPT.	4
(TRANSPOSABLE ELEMENT NEAR5 AMPLIF$).DWPI,USPT,EPAB,JPAB.	13

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09/622353

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                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

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FILE 'MEDLINE' ENTERED AT 12:44:31 ON 26 JUN 2002

=> s transposable element (10a)(isolat? or identif?)
L1          571 TRANSPOSABLE ELEMENT (10A)(ISOLAT? OR IDENTIF?)

=> l1 and amplif?
L1 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
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=> s l1 and amplif?
L2           67 L1 AND AMPLIF?

=> s l2 and adaptor#
L3            4 L2 AND ADAPTOR#

=> d l3 bib ab kwic 1-4

L3   ANSWER 1 OF 4  USPATFULL
AN     2002:22133  USPATFULL
TI     Novel drosophila tumor necrosis factor class molecule ("DmTNF") and
       variants thereof
IN     Carroll, Pamela M., Princeton, NJ, UNITED STATES
       Chen, Jian, Princeton, NJ, UNITED STATES
       Ramanathan, Chandra S., Wallingford, CT, UNITED STATES
       Xiao, Hong, Princeton Junction, NJ, UNITED STATES
       Guan, Bo, Princeton, NJ, UNITED STATES
       Bowen, Michael A., Lawrenceville, NJ, UNITED STATES
PI     US 2002012968      A1   20020131
AI     US 2001-813329     A1   20010320 (9)
PRAI   US 2000-190816P     20000321 (60)
DT     Utility
FS     APPLICATION
LREP   MARLA J MATHIAS, BRISTOL-MYERS SQUIBB COMPANY, PATENT DEPARTMENT, P O
       BOX 4000, PRINCETON, NJ, 08543-4000
CLMN   Number of Claims: 40
ECL    Exemplary Claim: 1
DRWN   18 Drawing Page(s)
LN.CNT 9244
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The present invention provides novel polynucleotides encoding Drosophila
       DmTNF polypeptides, fragments and homologs thereof. The present
       invention also is directed to novel polynucleotides encoding two
       Drosophila DmTNF variants, DmTNFv1 and DmTNFv2 polypeptides, fragments
       and homologs thereof. Also provided are vectors, host cells, antibodies,
```

and recombinant and synthetic methods for producing said polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of the polynucleotides and polypeptides of the present invention, in addition to methods of genetically modifying Drosophila or cultured cells to express or mis-express DmTNF, DmTNFv1, or DmTNFv2. The invention also relates to the use of such modified insects or cells to characterize DmTNF activity, identify TNF-like genes and/or genes implicated in modulating TNF, characterize TNF signaling pathways, and/or to identify modulators of DmTNF activity.

SUMM . . . cytoplasmice catalytic domains. TNF receptors interact with a family of molecules called TRAFs (TNF receptor associated proteins) that act as **adaptors** for the downstream signaling events. Hence, binding of a TNF cytokine to its cognate receptor, which is interacting with TRAF,. . .

DETD . . . using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or **amplifying** the corresponding gene from appropriate sources of genomic material.

DETD . . . the clone deposited with the ATCC, and/or the cDNA encoding the polypeptides of the present invention. PCR techniques for the **amplification** of nucleic acids are described in US Patent No. 4, 683, 195 and Saiki et al., Science, 239:487-491 (1988). PCR,. . . (if double-stranded), annealing of primer to target, and polymerization. The nucleic acid probed or used as a template in the **amplification** reaction may be genomic DNA, cDNA, RNA, or a PNA. PCR may be used to **amplify** specific sequences from genomic DNA, specific RNA sequence, and/or cDNA transcribed from mRNA. References for the general use of PCR. . .

DETD . . . a further round of transposase to induce excision of the element. Progeny in which the transposon has excised are typically **identified** by loss of the eye color marker associated with the **transposable element**. The resulting progeny will include flies with either precise or imprecise excision of the P element, where the imprecise excision. . .

DETD . . . be isolated. In one method, the activation domain sequences or DNA-binding domain sequences (depending on the prey hybrid used) are **amplified**, for example, by PCR using pairs of oligonucleotide primers specific for the coding region of the DNA binding domain or. . .

DETD . . . synthesis of overlapping oligonucleotides containing portions of the sequence encoding the antibody, annealing and ligating of those oligonucleotides, and then **amplification** of the ligated oligonucleotides by PCR.

DETD . . . tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention) by PCR **amplification** using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe. . . specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. **Amplified** nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the. . .

DETD [0370] The expression levels of an antibody molecule can be increased by vector **amplification** (for a review, see Bebbington and Hentschel, The use of vectors based on gene **amplification** for the expression of cloned genes in mammalian cells in DNA cloning, Vol.3. (Academic Press, New York, 1987)). When a marker in the vector system expressing antibody is **amplifiable**, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the **amplified** region is associated with the antibody gene, production of the antibody will also increase (Crouse et al., Mol. Cell. Biol.. . .

DETD . . . material (e.g., heterologous polynucleotide sequences) that is operably associated with the polynucleotides of the invention, and which activates, alters, and/or **amplifies** endogenous

polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter. . .

DETD . . . to real-time quantititive PCR using a PE 5700 instrument (Applied Biosystems, Foster City, Calif.) which detects the amount of DNA **amplified** during each cycle by the fluorescent output of SYBR green, a DNA binding dye specific for double strands. Reverse trancription. . .

DETD . . . performing the PCR with a first strand made with and without reverse transcriptase. In all cases, the contribution of material **amplified** in the reverse transcriptase controls was negligible. Small variations in the amount of cDNA used in each tube was determined. . .

DETD . . . upstream T7 RNA polymerase binding site and downstream DmTNF gene sequences could be designed such that the sequence could be **amplified** in a manner that would allow the generation of a DmTNF-derived dsRNA. PCR reactions could be performed using EXPAND High Fidelity (Boehringer Mannheim, Indianapolis, Ind.), for example, and the **amplified** products then purified.

DETD . . . are available to one skilled in the art for creating such mutants. Such methods may include a combination of PCR **amplification** and gene cloning methodology. Although one of skill in the art of molecular biology, through the use of the teachings. . .

DETD . . . 5' and 3' positions of SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5 may be designed to PCR **amplify**, and subsequently clone, the intended N- and/or C-terminal deletion mutant. Such primers could comprise, for example, an inititation and stop. . . 5' and 3' primer, respectively. Such primers may also comprise restriction sites to facilitate cloning of the deletion mutant post **amplification**. Moreover, the primers may comprise additional sequences, such as, for example, flag-tag sequences, kozac sequences, or other sequences discussed and/or. . .

DETD . . . example, in the case of the DmTNF 153 to V409 N-terminal deletion mutant, the following primers could be used to **amplify** a cDNA fragment corresponding to this deletion mutant:

5' Primer 5'-GCAGCAGCGGCCGCATTCTCGCACTAACGATCTGGCAG-3'
(SEQ ID NO:22)
NotI

3' Primer 5'-GCAGCAGTCGACCACCTTGAAGATGCCAAAGTAGC-3'
(SEQ ID. . .

DETD . . . example, in the case of the DmTNF M1 to V315 C-terminal deletion mutant, the following primers could be used to **amplify** a cDNA fragment corresponding to this deletion mutant:

5' Primer 5'-GCAGCAGCGGCCGCATGACTGCCGAGACCCTCAAGCCG-3'
(SEQ ID NO:24)
NotI

3' Primer 5'-GCAGCAGTCGACTACGCCATCGCGCGTTTGAAAGTG-3'
(SEQ ID. . .

DETD . . . example, in the case of the DmTNFv1 I53 to V406 N-terminal deletion mutant, the following primers could be used to **amplify** a cDNA fragment corresponding to this deletion mutant:

5' Primer 5'-GCAGCAGCGGCCGCATTCTCGCACTAACGATCTGGCAG-3'
(SEQ ID NO:22)
NotI

3' Primer 5'-GCAGCAGTCGACCACCTTGAAGATGCCAAAGTAGC-3'
(SEQ ID. . .

DETD . . . example, in the case of the DmTNFv1 M1 to V312 C-terminal deletion mutant, the following primers could be used to **amplify**

a cDNA fragment corresponding to this deletion mutant:

5' Primer 5'-GCAGCAGCGGCCGCATGACTGCCGAGACCCTCAAGCCG-3'
(SEQ ID NO:24)
NotI

3' Primer 5'-GCAGCAGTCGACGACGCCATCGCGCGTTTGAAAGTG-3'
(SEQ ID. . .

DETD . . . example, in the case of the DmTNFv2 I53 to V409 N-terminal deletion mutant, the following primers could be used to **amplify** a cDNA fragment corresponding to this deletion mutant:

5' Primer 5'-GCAGCAGCGGCCGCATTCTCGCACTAACGATCTGGCAG-3'
(SEQ ID NO:22)
NotI

3' Primer 5'-GCAGCAGTCGACCACCTTGAAGATGCCAAAGTAGC-3'
(SEQ ID. . .

DETD . . . example, in the case of the DmTNFv2 M1 to L316 C-terminal deletion mutant, the following primers could be used to **amplify** a cDNA fragment corresponding to this deletion mutant:

5' 5'-GCAGCAGCGGCCGCATGACTGCCGAGACCCTCAAGCCG-3' (SEQ ID NO:24)
Primer NotI

3' 5'-GCAGCAGTCGACCAAGACGCCATCGCGCGTTTGAAAG-3' (SEQ ID NO:25)
Primer SalI

DETD [0624] Representative PCR **amplification** conditions are provided below, although the skilled artisan would appreciate that other conditions may be required for efficient **amplification**. A 100 ul PCR reaction mixture may be prepared using long of the template DNA (cDNA clone of K+betaM5), 200. . .

DETD [0633] The 5' primer sequence for **amplifying** any additional N-terminal deletion mutants may be determined by reference to the following formula:

DETD [0635] The 3' primer sequence for **amplifying** any additional N-terminal deletion mutants may be determined by reference to the following formula:

DETD . . . sequences, etc.). The skilled artisan would appreciate that modifications of the above nucleotide positions may be necessary for optimizing PCR **amplification**.

DETD [0637] The same general formulas provided above may be used in identifying the 5' and 3' primer sequences for **amplifying** any C-terminal deletion mutant of the present invention. Moreover, the same general formulas provided above may be used in identifying the 5' and 3' primer sequences for **amplifying** any combination of N-terminal and C-terminal deletion mutant of the present invention. The skilled artisan would appreciate that modifications of the above nucleotide positions may be necessary for optimizing PCR **amplification**.

DETD [0662] The resulting shuffled, assembled, and **amplified** product can be purified using methods well known in the art (e.g., Qiagen PCR purification kits) and then subsequently cloned. . .

DETD . . . by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to **amplify** the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine. . . 1 min; elongation at 72 degree C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The **amplified** product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The. . .

DETD [0691] A icblynucleotide encoding a polypeptide of the present invention is **amplified** using PCbnoligonucleotide primers corresponding

to the 5' and 3' ends of the DNA sequence the synthesize insertion fragments. The primers used to **amplify** the cDNA insert shoefed preferably contain restriction sites, such as Bam-HI and XbaI, at the 5' end of therorimers in order to clone the **amplified** product into the expression vector. For examare, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression. . .

DETD [0692] The- pQE-9 vector is digested with BamHI and XbaI and the **amplified** fragment te ligated into the pQE-9 vector maintaining the reading frame initiated at the bacter,S1 RBS. The ligation mixture is. . .

DETD [0700] A polynucleotide encoding a polypeptide of the present invention is **amplified** using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence to synthesize insertion fragments. The primers used to **amplify** the cDNA insert should preferably contain restriction sites at the 5' end of the primers in order to clone the **amplified** product into the expression vector. Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified elsewhere herein (if applicable), is **amplified** using the PCR protocol described in Example 9. If the naturally occurring signal sequence is used to produce the protein,. . .

DETD [0701] The **amplified** fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Calif.).. . .

DETD [0712] The transformed gene can also be **amplified** to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that. . . cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the **amplified** gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

DETD [0713] A polynucleotide of the present invention is **amplified** according to the protocol outlined in herein. If the naturally occurring signal sequence is used to produce the protein, the. . . sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.) The **amplified** fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Calif.).. . .

DETD [0714] The **amplified** fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and. . .

L3 ANSWER 2 OF 4 USPATFULL

AN 2002:16871 USPATFULL

TI Drosophila homologues of genes and proteins implicated in metabolism and methods of use

IN Seidel-Dugan, Cindy, Benicia, CA, UNITED STATES
Friedman, Lori, San Francisco, CA, UNITED STATES
Torpey, Justin, San Francisco, CA, UNITED STATES
Keegan, Kevin Patrick, San Leandro, CA, UNITED STATES
Heller, Jonathan C., San Francisco, CA, UNITED STATES
Stout, Thomas J., San Francisco, CA, UNITED STATES

PI US 2002009751 A1 20020124

AI US 2000-740046 A1 20001218 (9)

PRAI US 1999-172484P 19991217 (60)
US 1999-172482P 19991217 (60)
US 2000-178411P 20000127 (60)
US 2000-191881P 20000323 (60)
US 2000-192142P 20000323 (60)

DT Utility

FS APPLICATION

LREP JAN P. BRUNELLE, EXELIXIS, INC., 170 HARBOR WAY, P.O. BOX 511, SOUTH SAN FRANCISCO, CA, 94083-0511

CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 2801
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Novel nucleic acids that are homologs of genes implicated in metabolism and that have been isolated from Drosophila melanogaster are described. These nucleic acids and proteins can be used to genetically modify metazoan invertebrate organisms, such as insects and worms, or cultured cells, resulting in novel gene expression or mis-expression. The genetically modified organisms or cells can be used in screening assays to identify candidate compounds which are potential therapeutics that interact with gene products implicated in metabolism. They can also be used in methods for studying gene activity and identifying other genes that modulate the function of, or interact with, genes implicated in metabolism.
SUMM . . . can be used to generate loss-of-function phenotypes. Subject nucleic acid fragments are also useful as nucleic acid hybridization probes and replication/**amplification** primers. Certain "antisense" fragments, i.e. that are reverse complements of portions of the coding sequence of SEQ ID NOs:1, 3,. . .
SUMM . . . (PCR) can also be used to isolate nucleic acids of the subject where oligonucleotide primers representing fragmentary sequences of interest **amplify** RNA or DNA sequences from a source such as a genomic or cDNA library (as described by Sambrook et al., supra). Additionally, degenerate primers for **amplifying** homologs from any species of interest may be used. Once a PCR product of appropriate size and sequence is obtained,. . .
SUMM . . . be isolated. In one method, the activation domain sequences or DNA-binding domain sequences (depending on the prey hybrid used) are **amplified**, for example, by PCR using pairs of oligonucleotide primers specific for the coding region of the DNA binding domain or activation domain. Other known **amplification** methods can be used, such as ligase chain reaction, use of Q replicase, or various other methods described (see Kricka. . .
SUMM . . . a further round of transposase to induce excision of the element. Progeny in which the transposon has excised are typically **identified** by loss of the eye color marker associated with the **transposable element**. The resulting progeny will include flies with either precise or imprecise excision of the P element, where the imprecise excision. . .
DETD . . . a 13 nucleotide C-tail to hybridize to the G-tailed first strand cDNA. The double stranded cDNA was ligated with BstX1 **adaptors** and digested with Not1. The cDNA was then fractionated by size by electrophoresis on an agarose gel and the cDNA. . .
DETD . . . the method described by Bonaldo et al. (Genome Research (1996) 6:791-806). Biotinylated driver was prepared from the cDNA by PCR **amplification** of the inserts and allowed to hybridize with single stranded plasmids of the same library. The resulting double-stranded forms were. . .

L3 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2002 ACS
AN 2000:663268 CAPLUS
DN 133:247749
TI Identification of transposon-tagged genes by the random sequencing of Mutator-tagged DNA fragments from Zea mays
AU Hanley, Steven; Edwards, David; Stevenson, David; Haines, Stephen; Hegarty, Matthew; Schuch, Wolfgang; Edwards, Keith J.
CS IACR-Long Ashton Research Station, University of Bristol, Long Ashton, Bristol, BS41 9AF, UK
SO Plant Journal (2000), 23(4), 557-566
CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal

LA English
AB A universal **adaptor amplification** procedure was used to isolate random Mutator-tagged fragments from Mutator-active maize plants. Direct sequence characterization of 761 Mutator-tagged fragments indicated that a significant no. were homologous to sequences within the public databases. The ability of Mutator-tagged fragments to detect homol. was not related to the length of the sequence within the range 100-400 bp. However, fragments above this size did show an increased chance of detecting homol. to either expressed sequence tags or genes. Characterization of the insertion sites of the Mutator elements suggested that while it does target transcribed regions, Mutator does not appear to have any site preference within the transcription unit. Hybridization of previously unidentified Mutator-tagged fragments to arrayed cDNA libraries confirmed that many of these also showed homol. to transcribed regions of the genome. Examn. of back-crossed progeny confirmed that all the insertions examd. were germinal; however, in all but one case, selfing 5 individual Mutator-tagged lines failed to reveal an obvious phenotype. This study suggests that the random sequencing of Mutator-tagged fragments is capable of producing both a significant no. of interesting transposon-tagged genes and mutant plant lines, all of which could be extremely valuable in future gene discovery and functional genomics programs.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB A universal **adaptor amplification** procedure was used to isolate random Mutator-tagged fragments from Mutator-active maize plants. Direct sequence characterization of 761 Mutator-tagged fragments indicated that a significant no. were homologous to sequences within the public databases. The ability of Mutator-tagged fragments to detect homol. was not related to the length of the sequence within the range 100-400 bp. However, fragments above this size did show an increased chance of detecting homol. to either expressed sequence tags or genes. Characterization of the insertion sites of the Mutator elements suggested that while it does target transcribed regions, Mutator does not appear to have any site preference within the transcription unit. Hybridization of previously unidentified Mutator-tagged fragments to arrayed cDNA libraries confirmed that many of these also showed homol. to transcribed regions of the genome. Examn. of back-crossed progeny confirmed that all the insertions examd. were germinal; however, in all but one case, selfing 5 individual Mutator-tagged lines failed to reveal an obvious phenotype. This study suggests that the random sequencing of Mutator-tagged fragments is capable of producing both a significant no. of interesting transposon-tagged genes and mutant plant lines, all of which could be extremely valuable in future gene discovery and functional genomics programs.
IT **Transposable element**
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(Mu element; **identification** of transposon-tagged genes by the random sequencing of Mutator-tagged DNA fragments from Zea mays)

L3 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS
AN 1999:529294 CAPLUS
DN 131:140482
TI **Transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes
IN Arbuckle, John A.; Fox, Timothy W.; Meeley, Robert B.; Bowen, Benjamin A.; McElver, John A.
PA Pioneer Hi-Bred International, Inc., USA
SO PCT Int. Appl., 34 pp.
CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9941415	A1	19990819	WO 1999-US3196	19990216
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 9926794	A1	19990830	AU 1999-26794	19990216
PRAI	US 1998-74931P	P	19980217		
	WO 1999-US3196	W	19990216		

AB A method for the rapid **isolation** and **identification** of the DNA sequence of **transposable element**-tagged genes is provided. The method comprises a modified AFLP approach using a **transposable element**-anchored **amplification** to **identify** and clone an **amplification** product that is assocd. with a mutant phenotype. Once cloned, the **amplification** product of interest may be used to screen a cDNA library directly or may be sequenced and compared to available databases for sequence homol. A modification of this approach provides a method for the identification of the location of an addnl. type of insertion event into genomic DNA, more specifically transgene insertion into the genome of a host organism. A genomic DNA is isolated and fragmented, resulting in a DNA sample comprising a collection of DNA fragments. An **adaptor** sequence is attached to at least one of sid DNA fragments. The adapter-modified DNA fragments are **amplified** to yield an **amplification** product comprising the genomic insertion-derived sequence flanked by: (1) a transgene-derived sequence and, (2) an adapter-derived sequence, wherein said **amplification** employs at least 2 oligonucleotide primers with one of the primers selectively hybridizing under stringent hybridization conditions to the adapter sequence and the other primer selectively hybridizing under stringent conditions to the transgene-derived sequence. The **amplification** products are analyzed to identify the inserted locations of the transgene. The transposable element may comprise a terminal inverted repeat or member of the Mutator family. The method us exemplified to isolate and identify the novel gene known as the lazy (la1) gene of maize, which is involved in the gravitropism response.

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI **Transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes

AB A method for the rapid **isolation** and **identification** of the DNA sequence of **transposable element**-tagged genes is provided. The method comprises a modified AFLP approach using a **transposable element**-anchored **amplification** to **identify** and clone an **amplification** product that is assocd. with a mutant phenotype. Once cloned, the **amplification** product of interest may be used to screen a cDNA library directly or may be sequenced and compared to available databases for sequence homol. A modification of this approach provides a method for the identification of the location of an addnl. type of insertion event into genomic DNA, more specifically transgene insertion into the genome of a host organism. A genomic DNA is isolated and fragmented, resulting in a DNA sample comprising a collection of DNA fragments. An **adaptor** sequence is attached to at least one of sid DNA fragments. The adapter-modified DNA fragments are **amplified** to yield an **amplification** product comprising the genomic insertion-derived sequence flanked by: (1) a transgene-derived sequence and, (2) an adapter-derived sequence, wherein

said **amplification** employs at least 2 oligonucleotide primers with one of the primers selectively hybridizing under stringent hybridization conditions to the adapter sequence and the other primer selectively hybridizing under stringent conditions to the transgene-derived sequence. The **amplification** products are analyzed to identify the inserted locations of the transgene. The transposable element may comprise a terminal inverted repeat or member of the Mutator family. The method us exemplified to isolate and identify the novel gene known as the lazy (la1) gene of maize, which is involved in the gravitropism response.

ST transposable element anchored **amplification** tagged gene

IT Genetic polymorphism
(AFLP (**amplification** fragment length polymorphism); **transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes)

IT Nucleic acid **amplification** (method)
(DNA; **transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes)

IT **Transposable element**
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(Mu element; **transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes)

IT PCR (polymerase chain reaction)
(TAIL (thermal asym. interlaced)-PCR; **transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes)

IT Repetitive DNA
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(inverted, terminal; **transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes)

IT Corn
(lazy gene from; **transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes)

IT Gene, plant
RL: ANT (Analyte); ANST (Analytical study)
(lazy; **transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes)

IT Gene
RL: ANT (Analyte); ANST (Analytical study)
(**transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes)

IT Primers (nucleic acid)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(**transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes)

IT **Transposable element**
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(**transposable element**-anchored **amplification** method for **isolation** and **identification** of tagged genes)

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L4            0 TRANPOSABLE ELEMENT#(P) ADAPTOR(P) AMPLIF?

=> s transposable element(P)adaptor#(P)amplif?
L5            1 TRANSPOSABLE ELEMENT(P) ADAPTOR#(P) AMPLIF?

=> d l5 bib ab kwic

L5   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2002 ACS
AN   1999:529294  CAPLUS
DN   131:140482
TI   Transposable element-anchored amplification method for isolation and
     identification of tagged genes
IN   Arbuckle, John A.; Fox, Timothy W.; Meeley, Robert B.; Bowen, Benjamin A.;
     McElver, John A.
PA   Pioneer Hi-Bred International, Inc., USA
SO   PCT Int. Appl., 34 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   WO 9941415         A1   19990819       WO 1999-US3196   19990216
         W:  AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
             DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE,
             KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW,
             MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR,
             TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
             FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
             CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     AU 9926794         A1   19990830       AU 1999-26794    19990216
PRAI US 1998-74931P     P    19980217
     WO 1999-US3196     W    19990216
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RE.CNT  5     THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
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